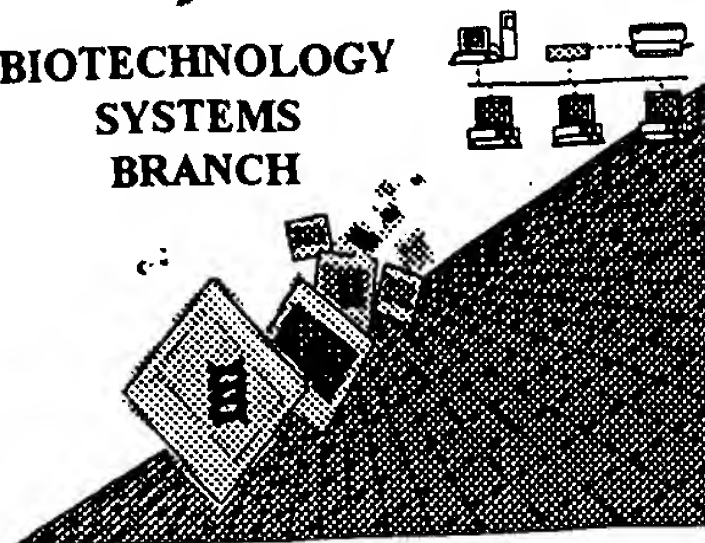


0280

RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/823,886

Source: OIPF

Date Processed by STIC: 4/18/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/823,886

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) . Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000
- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of "Artificial" Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
(NEW RULES) Valid response is Artificial Sequence.
- 12 Use of <220>Feature Sequence(s) 16 are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
 Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIEP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/823,886

DATE: 04/18/2001
TIME: 07:51:31

Input Set : A:\C1102-7002.txt
Output Set: N:\CRF3\04182001\I823886.raw

Does Not Comply
Corrected Diskette Needed
P.6

3 <110> APPLICANT: Newell, Martha
4 Berry-Lowe, Sandra
6 <120> TITLE OF INVENTION: Compositions and methods for regulating metabolism in plants
8 <130> FILE REFERENCE: C1102/7002
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/823,886
11 <141> CURRENT FILING DATE: 2001-03-30
13 <150> PRIOR APPLICATION NUMBER: US 60/193,533
14 <151> PRIOR FILING DATE: 2000-03-31
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17 <170> SOFTWARE: PatentIn version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 924
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
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29 ctccaggtcc aaggtgaatg cccgacgtcc agtggtatta ggtataaagg tgtcctggga 180
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49 attaatcttc caccaggaca gtacaaaagt gtgcccaact gtgcaatgaa agtggttact 780
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60 <212> TYPE: PRT
61 <213> ORGANISM: Homo sapiens
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67 Leu Phe Ser Ala Gly Ile Ala Ala Cys Leu Ala Asp Val Ile Thr Phe
68 20 25 30
70 Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Val Gln Gly Glu Cys Pro
71 35 40 45
73 Thr Ser Ser Val Ile Arg Tyr Lys Gly Val Leu Gly Thr Ile Thr Ala
74 50 55 60
76 Val Val Lys Thr Glu Gly Arg Met Lys Leu Tyr Ser Gly Leu Pro Ala
77 65 70 75 80
79 Gly Leu Gln Arg Gln Ile Ser Ser Ala Ser Leu Arg Ile Gly Leu Tyr

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/823,886

DATE: 04/18/2001

TIME: 07:51:31

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Output Set: N:\CRF3\04182001\I823886.raw

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83          100          105          110
85 Leu Gly Ser Lys Ile Leu Ala Gly Leu Thr Thr Gly Gly Val Ala Val
86          115          120          125
88 Phe Ile Gly Gln Pro Thr Glu Val Val Lys Val Arg Leu Gln Ala Gln
89          130          135          140
91 Ser His Leu His Gly Ile Lys Pro Arg Tyr Thr Gly Thr Tyr Asn Ala
92 145          150          155          160
94 Tyr Arg Ile Ile Ala Thr Thr Glu Gly Leu Thr Gly Leu Trp Lys Gly
95          165          170          175
97 Thr Thr Pro Asn Leu Met Arg Ser Val Ile Ile Asn Cys Thr Glu Leu
98          180          185          190
100 Val Thr Tyr Asp Leu Met Lys Glu Ala Phe Val Lys Asn Asn Ile Leu
101          195          200          205
103 Ala Asp Asp Val Pro Cys His Leu Val Ser Ala Leu Ile Ala Gly Phe
104          210          215          220
106 Cys Ala Thr Ala Met Ser Ser Pro Val Asp Val Val Lys Thr Arg Phe
107 225          230          235          240
109 Ile Asn Ser Pro Pro Gly Gln Tyr Lys Ser Val Pro Asn Cys Ala Met
110          245          250          255
112 Lys Val Phe Thr Asn Glu Gly Pro Thr Ala Phe Phe Lys Gly Leu Val
113          260          265          270
115 Pro Ser Phe Leu Arg Leu Gly Ser Trp Asn Val Ile Met Phe Val Cys
116          275          280          285
118 Phe Glu Gln Leu Lys Arg Glu Leu Ser Lys Ser Arg Gln Thr Met Asp
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121 Cys Ala Thr
122 305
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125 <211> LENGTH: 1105
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127 <213> ORGANISM: Homo sapiens
129 <400> SEQUENCE: 3
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132 tcttgggacg tagcaggaaa tcagcatcat ggttgggttc aaggccacag atgtgcccc 120
134 tactgccact gtgaagtttc ttggggctgg cacagctgcc tgcctcgcag atctcatcac 180
136 ctttcctctg gatactgcta aagtccggtt acagatccaa ggagaaagtc aggggccagt 240
138 gcgcgtaca gccagcgccc agtaccgcgg tgtgatgggc accattctga ccatggtgcg 300
140 tactgagggc ccccgaaagg tctacaatgg gctggttgcc ggcctgcagc gccaaatgag 360
142 ctttgccctc gtccgcacgc gcctgtatga ttctgtcaaa cagttctaca ccaagggctc 420
144 tgagcatgcc agcattggga gccgcctcct agcaggcagc accacaggtg ccctggctgt 480
146 ggctgtggcc cagcccacgg atgtggtaaa ggtccgattc caagctcagg cccgggctgg 540
148 aggtggtcgg agataccaaa gcaccgtcaa tgcttacaag accattgccg gagaggaagg 600
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154 agatgacctc ccttgccact tcactttctgc ctttggggca ggcttctgca ccactgtcat 780
156 cgcctcccct gtagacgtgg tcaagacgag atacatgaac tctgccctgg gccagtacag 840
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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/823,886

DATE: 04/18/2001

TIME: 07:51:31

Input Set : A:\C1102-7002.txt

Output Set: N:\CRF3\04182001\I823886.raw

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166 ttcttcttcc tttctcttcc ctccg 1105
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170 <211> LENGTH: 314
171 <212> TYPE: PRT
172 <213> ORGANISM: Homo sapiens
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179 Thr Ala Thr Val Lys Phe Leu Gly Ala Gly Thr Ala Ala Cys Ile Ala
180 20 25 30
182 Asp Leu Ile Thr Phe Pro Leu Asp Thr Ala Lys Val Arg Leu Gln Ile
183 35 40 45
185 Gln Gly Glu Ser Gln Gly Pro Val Arg Ala Thr Ala Ser Ala Gln Tyr
186 50 55 60
188 Arg Gly Val Met Gly Thr Ile Leu Thr Met Val Arg Thr Glu Gly Pro
189 65 70 75 80
191 Arg Ser Leu Tyr Asn Gly Leu Val Ala Gly Leu Gln Arg Gln Met Ser
192 85 90 95
194 Phe Ala Ser Val Arg Ile Gly Leu Tyr Asp Ser Val Lys Gln Phe Tyr
195 100 105 110
197 Thr Lys Gly Ser Glu His Ala Ser Ile Gly Ser Arg Leu Leu Ala Gly
198 115 120 125
200 Ser Thr Thr Gly Ala Leu Ala Val Ala Val Ala Gln Pro Thr Asp Val
201 130 135 140
203 Val Lys Val Arg Phe Gln Ala Gln Ala Arg Ala Gly Gly Gly Arg Arg
204 145 150 155 160
206 Tyr Gln Ser Thr Val Asn Ala Tyr Lys Thr Ile Ala Arg Glu Glu Gly
207 165 170 175
209 Phe Arg Gly Leu Trp Lys Gly Thr Ser Pro Asn Val Ala Arg Asn Ala
210 180 185 190
212 Ile Val Asn Cys Ala Glu Leu Val Thr Tyr Asp Leu Ile Lys Asp Ala
213 195 200 205
215 Leu Leu Lys Ala Asn Leu Met Thr Asp Asp Leu Pro Cys His Phe Thr
216 210 215 220
218 Ser Ala Phe Gly Ala Gly Phe Cys Thr Thr Val Ile Ala Ser Pro Val
219 225 230 235 240
221 Asp Val Val Lys Thr Arg Tyr Met Asn Ser Ala Leu Gly Gln Tyr Ser
222 245 250 255
224 Ser Ala Gly His Cys Ala Leu Thr Met Leu Gln Lys Glu Gly Pro Arg
225 260 265 270
227 Ala Phe Tyr Lys Gly Phe Met Pro Ser Phe Leu Arg Leu Gly Ser Trp
228 275 280 285
230 Asn Val Val Met Phe Val Thr Tyr Glu Gln Leu Lys Arg Ala Leu Met
231 290 295 300
233 Ala Ala Cys Thr Ser Arg Glu Ala Pro Phe
234 305 310

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/823,886

DATE: 04/18/2001

TIME: 07:51:31

Input Set : A:\C1102-7002.txt

Output Set: N:\CRF3\04182001\I823886.raw

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237 <211> LENGTH: 1132
238 <212> TYPE: DNA
239 <213> ORGANISM: Homo sapiens
241 <400> SEQUENCE: 5
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244 ccaccgctgc actgaagccc agggctgtgg agcagcctct ctcccttgac ctccctctcg 120
246 ccctaaaggg actgggcaga gccttccagg actatggttg gactgaagcc ttcagacgtg 180
248 cctcccacca tggctgtgaa gttcctgggg gcaggcacag cagcctgttt tgctgacctc 240
250 gttacctttc cactggacac agccaaggtc cgctgcaga tccaggggga gaaccaggcg 300
252 gtccagacgg cccggctcgt gcagtaccgt ggcgtgctgg gcaccatcct gaccatggtg 360
254 cggactgagg gtccctgcag cccctacaat gggctggtgg ccggcctgca gcgccagatg 420
256 agcttcgcct ccattccgat cggcctctat gactccgtca agcaggtgta ccccccaaa 480
258 ggcgcggaca actccagcct cactaccogg attttggccg gctgcaccac aggagccatg 540
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262 ctggggccat ccaggagcga cagaaaatac agcgggacta tggacgccta cagaaccatc 660
264 gccagggagg aaggagtcag gggcctgtgg aaaggaactt tgcccaacat catgaggaat 720
266 gctatcgtca actgtgctga ggtggtgacc tacgacatcc tcaaggagaa gctgctggac 780
268 taccacctgc tcaactgaaa cttcccctgc cactttgtct ctgccttttg agccggcttc 840
270 tgtgccacag tgggtggcctc cccggtggac gtggtgaaga cccggtatat gaactcacct 900
272 ccaggccagt acttcagccc cctcgactgt atgataaaga tgggtggocca ggaggggccc 960
274 acagccttct acaaggggtg agcctcctcc tgcctccagc actccctccc agagaacagg 1020
276 ggcttctttc ttttcgaatg tggctaccgt gggtaaacct gggatgtagc ggtgaagagt 1080
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283 <212> TYPE: PRT
284 <213> ORGANISM: Homo sapiens
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289 1 5 10 15
291 Asp Val Pro Pro Thr Met Ala Val Lys Phe Leu Gly Ala Gly Thr Ala
292 20 25 30
294 Ala Cys Phe Ala Asp Leu Val Thr Phe Pro Leu Asp Thr Ala Lys Val
295 35 40 45
297 Arg Leu Gln Ile Gln Gly Glu Asn Gln Ala Val Gln Thr Ala Arg Leu
298 50 55 60
300 Val Gln Tyr Arg Gly Val Leu Gly Thr Ile Leu Thr Met Val Arg Thr
301 65 70 75 80
303 Glu Gly Pro Cys Ser Pro Tyr Asn Gly Leu Val Ala Gly Leu Gln Arg
304 85 90 95
306 Gln Met Ser Phe Ala Ser Ile Arg Ile Gly Leu Tyr Asp Ser Val Lys
307 100 105 110
309 Gln Val Tyr Thr Pro Lys Gly Ala Asp Asn Ser Ser Leu Thr Thr Arg
310 115 120 125
312 Ile Leu Ala Gly Cys Thr Thr Gly Ala Met Ala Val Thr Cys Ala Gln
313 130 135 140
315 Pro Thr Asp Val Val Lys Val Arg Phe Gln Ala Ser Ile His Leu Gly
316 145 150 155 160

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/823,886

DATE: 04/18/2001

TIME: 07:51:31

Input Set : A:\C1102-7002.txt

Output Set: N:\CRF3\04182001\I823886.raw

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322                               180                               185                               190
324 Pro Asn Ile Met Arg Asn Ala Ile Val Asn Cys Ala Glu Val Val Thr
325                               195                               200                               205
327 Tyr Asp Ile Leu Lys Glu Lys Leu Leu Asp Tyr His Leu Leu Thr Asp
328                               210                               215                               220
330 Asn Phe Pro Cys His Phe Val Ser Ala Phe Gly Ala Gly Phe Cys Ala
331 225                               230                               235                               240
333 Thr Val Val Ala Ser Pro Val Asp Val Val Lys Thr Arg Tyr Met Asn
334                               245                               250                               255
336 Ser Pro Pro Gly Gln Tyr Phe Ser Pro Leu Asp Cys Met Ile Lys Met
337                               260                               265                               270
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340                               275                               280
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343 <211> LENGTH: 6428
344 <212> TYPE: DNA
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347 <400> SEQUENCE: 7
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350 gaaatataaa agagaaagag tggaagaaaa gatgagaaat attatattgt gtatattgag      120
352 taagtgtagt gaacgagaga gttgagacag agaaaatatt ttaagtcttt aactatatct      180
354 actatacaaa ggagaatatt catatgttga aggaaagtgt tcttgtgtgg agttttggac      240
356 tcttcaacta attcagagtt gtacaacggt attggactat tgtatcctgg agaggacaag      300
358 tcaagagtga tactgctgga tcggtgtaga ttatgccgta gttgacttga atcttcttaa      360
360 agagagttag atattcgtgc ctcaagtctaa aaatttgttt attcattttt gtcattttat      420
362 tttcaactat aatattttgt atttgtggta tattacactg ccttatcatg ataatcatcg      480
364 tgattttctaa ctagatcatg acgtctcaat taaatgtttt ctccaacta aacacatccc      540
366 atattttatat tattcgacat tgggttaatt gattatttat cccactttta gcctatgcac      600
368 aggggtag ctatgttaaa gtcagggtgt taaattgaat atccttcgtc aaaaactaat      660
370 atcatattta tgtaaaatta tatacgaagt gattaaataa catattttgg acattcttaa      720
372 cagaacaagg tgttgttgcc caatcgtttc attatttctg tcacaattaa caaatctacc      780
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376 ggaaagagta acgtttacgc atccttaata aaatgttaga tgatgaatga ggatctaata      900
378 agcatatgtg caaagctcca accaatcatg attatctaata aaagtgtgct ttattcatta      960
380 ttctaaaatt caacaattaa taaaataatt aggtcaaaag cacatgggtg agtggatgag      1020
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384 ttattagggt ctatttaatt tctcgtatct gatatttgca ttaaaattca attaatattg      1140
386 attcacatga tataaaaccc caatcacact actcgaattt aaaaccttta attaagggga      1200
388 gtaacaattg aataacaaaa aaaaatctgt tgggagtgcc acccccgaat agaccctgta      1260
390 gagcgcgatt caaatttaac cgaaactcta atgtgggctc cgagaaacaa aaaaaaaaaa      1320
392 caattgaata gcaaaggaaa acagagtagt gctgactgag caagcaaaag cccaattgaa      1380
394 atattagtag taaatgacag caatggccgt tgcgtaggac aagcacagca gcagccccgt      1440
396 tttcgtcttt cccaagatct ctctgcaaaa tccttagcct tctttactat ataatagccc      1500
398 ctaaaacccc attttttact ataccatttt cttactcttg ctctgtgatc atcctttctt      1560
400 ctaggagtag ccatctccta gaaccctttt agtttctctt tgtgtttttt tggatcaattt      1620
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<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<221> Artificial Sequence

<222> (1)..(27)

<400> 16

cttgccatc tcgagcatgc aggcac

see item 12 on Eno Summary Sheet

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/823,886

DATE: 04/18/2001

TIME: 07:51:32

Input Set : A:\C1102-7002.txt

Output Set: N:\CRF3\04182001\I823886.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:15 M:283 W: Missing Blank Line separator, <160> field identifier
L:62 M:283 W: Missing Blank Line separator, <400> field identifier
L:663 M:283 W: Missing Blank Line separator, <400> field identifier
L:744 M:283 W: Missing Blank Line separator, <400> field identifier
L:806 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:821 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:836 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:851 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
L:854 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: